

Fig. S1. *Hoxd9,10,11* expression in the adult uterus. Immunofluorescent staining for HOXD9,10,11 in cross-sections of uteri from WT ovariectomized mice treated with oil, progesterone (P4) or estrogen (E2) and untreated *Hoxd9,10,11*^{-/-} mice. Expression of all three genes is similar and found in the luminal epithelium of oil-treated controls and shifts to the glandular epithelium in response to P4.

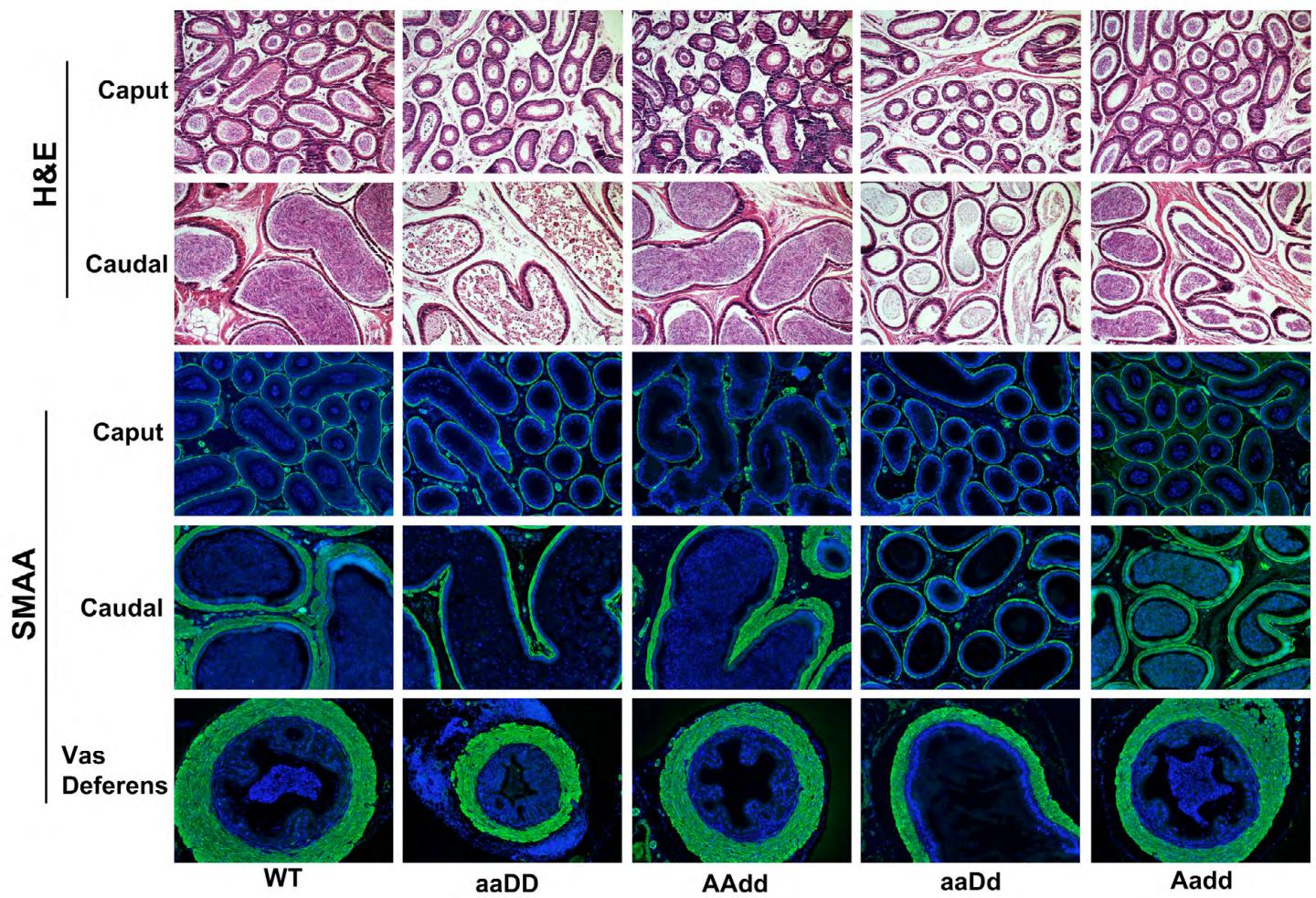


Fig. S2. ACTA2 staining in WT and Hox mutant male reproductive tracts. Immunofluorescent staining for ACTA2 in cross-sections of WT and Hox mutant vas deferens and the caput and caudal sections of epididymis show thinning of muscle in *Hoxa9,10,11^{-/-}* tissues. The absence of DAPI staining in the lumen of the *Hoxa9,10,11^{-/-}* epididymis confirms the failure of spermatogenesis in these mice, and this is shown more clearly in H&E-stained sections. Note the smaller tubules of the *Hoxa9,10,11^{-/-}* *d9,10,11^{+/-}* caudal epididymis, which resemble the more anterior caput and suggest anteriorization extending into the epididymis.

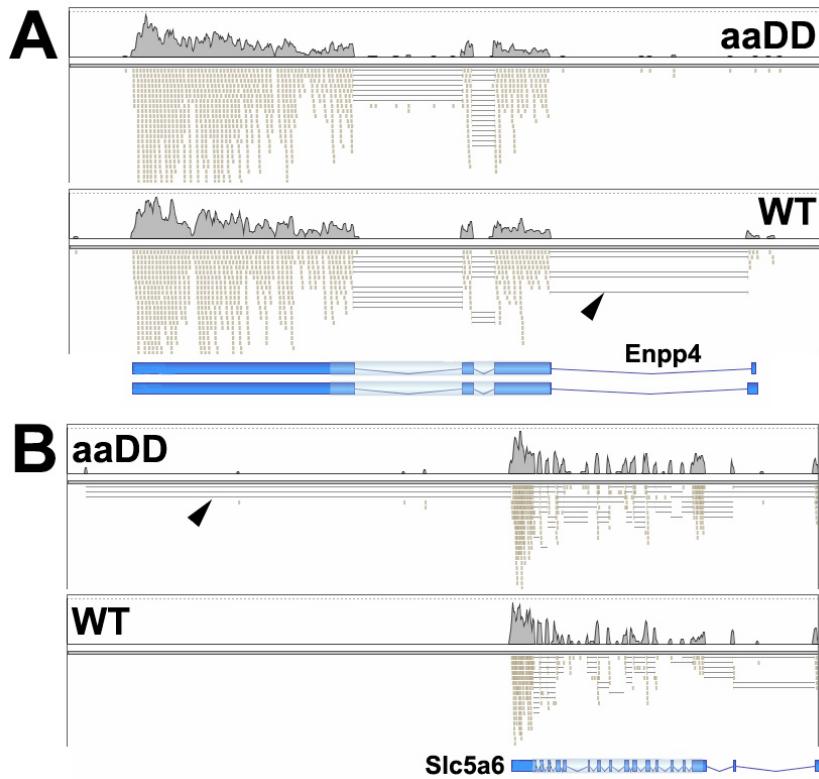


Fig. S3. Examples of differential splicing detected by RNA-Seq in *Hoxa9,10,11*^{-/-} versus WT uteri. RNA-Seq reads (tan dots) and splicing events (lines) from *Hoxa9,10,11*^{-/-} and WT uteri for the genes (A) *Enpp4* and (B) *Slc5a6*. Arrowheads show differential splicing events. For *Enpp4* there is inclusion of a known exon in the WT uterus that is not present in the *Hoxa9,10,11*^{-/-} uterus despite similar levels of expression for this gene. For *Slc5a6* there is inclusion of a previously unannotated exon in the *Hoxa9,10,11*^{-/-} uterus that is not present in the WT uterus.

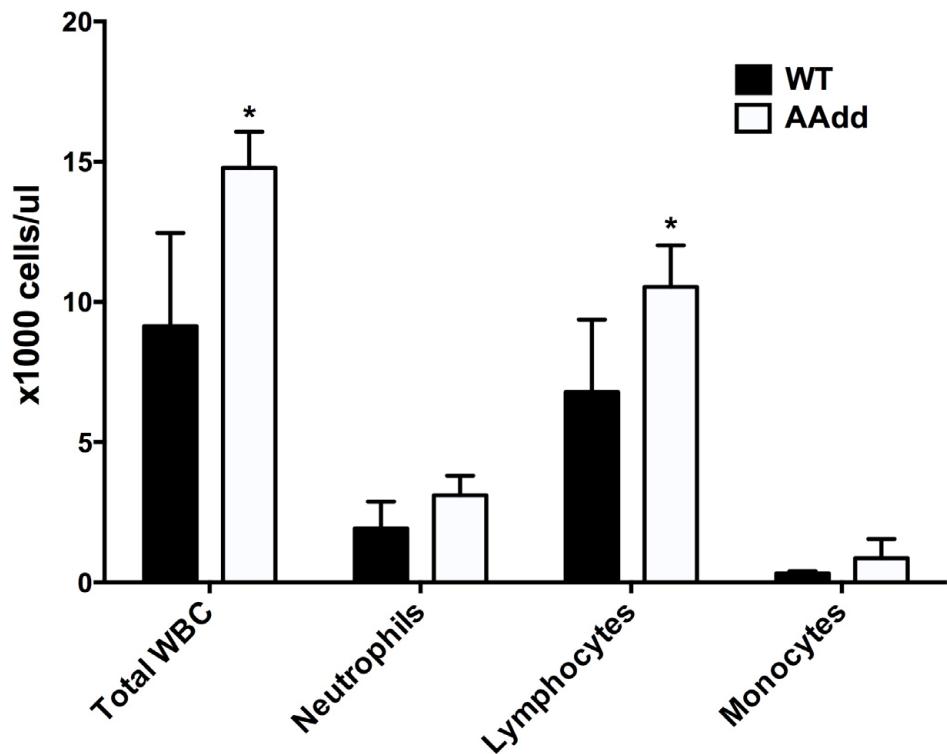


Fig. S4. Increased leukocyte populations in the peripheral blood of *Hoxd9,10,11*^{-/-} versus WT females. Hemavet analysis of peripheral blood from *Hoxd9,10,11*^{-/-} and WT females ($n=4$) showed significant increases in total white blood cells and lymphocytes, with trends towards increased neutrophil and monocyte populations.

Table S1. Sequence and primer information**pl451 modified for recombineering (4860 bp)**

1	CTAAATTGTA AGCGTTAATA TTTTGTAAA ATTTCGCGTTA AATTTTGTT AAATCAGCTC
61	ATTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTAT AAATCAAAAG AATAGACCGA
121	GATAGGGTTG AGTGTGTTTC CAGTTGGAA CAAGAGTCCA CTATTAAAGA ACGTGGACTC
181	CAACGTCAAA GGGCGAAAAAA CCGTCTATCA GGGCGATGGC CCACTACGTG AACCATCACC
241	CTAATCAAGT TTTTGCGGGT CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG
301	CCCCCGATT AGAGCTTGAC GGGGAAAGCC GGCGAACGTG GCGAGAAAGG AAGGGAAGAA
361	AGCGAAAGGA GCAGGCCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC GCGTAACCAC
421	CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTCC CATTGCCAT TCAGGCTGCG
481	CAACTGTTGG GAAGGGCGAT CGGTGCGGGC CTCTTCGCTA TTACGCCAGC TGGCGAAAGG
541	GGGATGTGCT GCAAGGCGAT TAAGTTGGGT AACGCCAGGG TTTTCCCAGT CACGACGTTG
601	TAAAACGACG GCCAGTGAAT TGTAAATACGA CTCACTATAG GGCGAATTGG GTACCGGGCC
661	CCCCCTCGAG GTCGACGGTA TCGATAAGCT TTACCGTTCG TATAGCATAAC ATTATACGAA
721	GTTATGAATT CCGAAGTTCC TATTCTCTAG AAAGTATAGG AACTTCAGGT CTGAAGAGGA
781	GTTTACGTCC AGCCAAGCTA GCTTGGCTGC AGGTCGTCGA AATTCTACCG GGTAGGGGAG
841	GCGCTTTCC CAAGGCAGTC TGGAGCATGC GCTTAGCAG CCCCCTGGG CACTTGGCGC
901	TACACAAGTG GCCTCTGGCC TCGCACACAT TCCACATCCA CCGTAGGCG CCAACCGGCT
961	CCGTTCTTG GTGGCCCTT CGCGCCACCT TCTACTCCTC CCCTAGTCAG GAAGTTCCCC
1021	CCCGCCCCGC AGCTCGCGTC GTGCAGGACG TGACAAATGG AAGTAGCACG TCTCACTAGT
1081	CTCGTGCAGA TGGACAGCAC CGCTGAGCAA TGGAAGCGGG TAGGCCTTTG GGGCAGCGGC
1141	CAATAGCAGC TTTGCTCCTT CGCTTTCTGG GCTCAGAGGC TGGGAAGGGGG TGGGTCCGGG
1201	GGCGGGCTCA GGGGCGGGCT CAGGGGCGGG GCGGGCGCCC GAAGGTCCCTC CGGAGGCCG
1261	GCATTCTGCA CGCTTCAAAA GCGCACGTCT GCCGCGCTGT TCTCCTCTTC

Table S2. Genes co-regulated in Hox mutant uteri by microarray

[Download Table S2](#)

Table S3. Genes co-regulated in Hox mutant vas deferens by microarray

[Download Table S3](#)

Table S4. Overlap of microarray and RNA-Seq data in *Hoxa9,10,11* and *Hoxd9,10,11* mutant versus WT uteri

[Download Table S4](#)

Table S5. Functional enrichment of genes altered in Hox mutant uteri

[Download Table S5](#)